

GGGTGAGGGGAGGAGCCCGAGGACCTTTCTGGGGCGCTGGGGGATCCTCTTGCACTGGTGGGTGGA  
GAGAAGCGCCTGCAGCCAACCAGGGTCAAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAA  
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC  
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA  
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCC'  
CTGTGGAGGCAGAGCCAGTGGAGCCCAGTGAAGCAGGGCTGCTTGGCAGCCACCGGCCTGCA  
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCGCTGACGGCCAGGGTGAAGCATG  
TGAGGAGCCGCCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTTCATAGATTCTATTACAAAGA  
ATAACCACCATTTTTGAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG  
CTGGCTGCCATGGGAGCTGTTGCAAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC  
GCCAAGAGAGTTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA  
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG  
CCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT  
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG  
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC  
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAGCT  
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC  
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATCGCGCAG  
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCCCCCGCTGC  
CCCCCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG  
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC  
ACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCCATGGAGAGACTGCCTGCAGGCCCT  
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA  
TGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG  
GATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTTGGGAACATTGA  
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC  
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC  
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA  
CTCCTTTACATGGCACAACGGCAAGCAGTTACCAACCTGGACAGAGATCATGATGTCTACA  
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC  
CTCAACGGGGTCTGGTACC GCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG  
GGCTGAGTTCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC  
CCAACACCTTCCACTAAGCCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCC  
CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGAGGCTGGGA  
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACCTGAATCGAT  
ACGGTGTTTTTCTGTCCCTCCTACTTTCTTACACCAGACAGCCCCCTCATGTCTCCAGGACA  
GGACAGGACTACAGACAACCTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAAA

## FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
Q RVTGAICVNSKEPEVLLNVRVHKQELELLNNELLKQKRQIETLQQLV EVDGGIVSEVKLLR
KESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTLADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFFRNWETKYQGFGNIDGEYWLGLENIYWLTNQGNKYKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-22

#### N-glycosylation sites.

amino acids 164-168, 192-196

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

#### Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

#### N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,  
465-471, 473-479

#### Amidation site.

amino acids 373-377

#### Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

#### Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

#### Trehalase proteins.

amino acids 275-292

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### **FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT  
GTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGGCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGAACACTGAAAACACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
GGCAGTAATACGGACTCTTGTTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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## **FIGURE 4**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDK

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-myristoylation sites.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

**FIGURE 5**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG  
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA  
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVRVLFSGSKKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA  
MNSEGILYTSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

### **N-glycosylation site.**

amino acids 242-246

### **Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

### **Tyrosine kinase phosphorylation site.**

amino acids 93-100

### **N-myristoylation site.**

amino acids 87-93, 231-237

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

### **HBGF/FGF family proteins**

amino acids 78-94, 102-153

**ATG**CGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

## **FIGURE 8**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIEGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDGTDKDDSTNSTLENLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT
```

### **N-glycosylation site.**

amino acids 100-104, 242-246

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

### **Tyrosine kinase phosphorylation site.**

amino acids 199-207

### **N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

### **HBGF/FGF family proteins.**

amino acids 104-155, 171-198



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**FIGURE 10**

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ  
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQ  
CVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPG  
SYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDM  
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG  
GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMATT  
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGS  
SVIRLRIYVSQYPF

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 283-287, 296-300

**N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,  
267-273, 310-316

**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

**Cell attachment sequence.**

amino acids 54-57

**Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

## FIGURE 11

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGAACACAGGTCCCTTGTGTGCTGCAGAGAAGCAGTTGTTTTGCTG  
GAAGGAGGGAGTGCGCGGGCTGCCCCGGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTT  
CCAGGCACCCTGTCTGGGGCAGGGAGGGACAGGCCTGCACATCGAAGGTGGGGTGGGACCA  
GGCTGCCCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTGCAGACTCTCA  
GGGCTAAGGTCCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT  
AGCTTGAAGGAGGCACC**ATG**CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG  
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG  
TGCCTACCGCGACCTAGAATCCGTGCCGCCTGGCTTCCCGGCCAATGTGACTACACTGAGCC  
TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCCTTCAGGGAGGTGCCCTTGCTGCAG  
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGAGCCCTGGCCTCTCTGAG  
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC  
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC  
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACAC  
ATTGGCCGAGGGCACCTTCACCCCGCTCACCGCGCTGTCCACCTGCAGATCAACGAGAACC  
CCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCCGTGTCC  
ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG  
CCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG  
ATGGTGCCGAGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGAGCCG  
GCCCCCTCAGCTTCACTGGCACATCCAGATAACCCAGTGGCATTGTGGAGATCACAGCCCCAA  
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCAGCCGCGCTTCC  
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC  
AGCTGCCTGGCCACCAATGAGCTGGGCAGCTGCTGAGAGCTCAGTGGACGTGGCACTGGCCAC  
GCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA  
AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC  
ATCTACCTCAGCCGTGCTGGGAACCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT  
GCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTCTTCTTCTTCTCCTCACCTCCTT**C**  
**AG**CCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCCCTACCAATGCCCTTTAAGTGCTG  
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCT  
CCTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAAACTAGTGA  
CTAGGATAGAATTTGATCCCCTAACCTACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTG  
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAACCTGGGAGAA  
GCCTCAGTGGTGGAATTCCAGGCACCTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA  
ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG  
GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT  
CCTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCCTCATCTGAGACTGAAA  
TGTGGGATCCAGGATGGCCTTCCTTCTCTTACCCTTCCTCCCTCAGCCTGCAACCTCTAT  
CCTGGAACCTGTCCTCCCTTTCTCCCCAACTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC  
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA  
AAGGGCGGCCGCGACTCTAGAGTCGACCT

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## **FIGURE 12**

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFANVTLSLSANRL  
PGLPEGAFFREVPLLQSLWLAHNEIRTVAAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL  
QLLKMSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTC  
GIVWLKTWALTAVSIPEDQNIACSTPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR  
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG  
SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHHGKAVEGKGCYTV  
DNEVQPSGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSTF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **Transmembrane domain:**

amino acids 403-418

#### **N-glycosylation sites.**

amino acids 51-55, 120-124, 309-313

#### **Tyrosine kinase phosphorylation site.**

amino acids 319-326

#### **N-myristoylation sites.**

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,  
334-340, 350-356, 394-400

#### **Amidation site.**

amino acids 355-359

#### **Leucine rich repeats.**

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

#### **Leucine rich repeat C-terminal domain.**

amino acids 180-230

## FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC  
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTCCC  
AGCGAGGAGGTCCTGAGCAGCATGCCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT  
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGAGGAGGAGA  
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC  
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAG  
AATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG  
CAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCA  
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT  
CCCATGTCTTGGAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT  
CTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA  
GCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG  
TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG  
GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT  
GACAAAGCAAAGTGTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG  
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC  
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCCAAAGGTTACCAGGGAGAC  
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA  
CAAATGCCAATGTCAAGAAGGTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC  
TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG  
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC  
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTTGAATGTTCAAATAA  
TGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT  
GATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT  
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAATTTTCAGTG  
TGAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT  
CAGAAAGGTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT  
TGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGATGTTTGTTACATTTTTTAAAAA  
TTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT  
CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTTAAACAATATAATATATTCTA  
AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA  
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT  
AAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 14**

MARRSAFFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK  
 MAPFTHDERKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLL  
 GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
 RGGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPPGFYGVNCDKANCST  
 TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC  
 EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
 PESNYIW

**Signal sequence.**

amino acids 1-28

**N-glycosylation sites.**

amino acids 88-92, 245-249

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338



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## **FIGURE 16**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAV  
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **N-myristoylation sites.**

amino acids 3-9, 26-32

#### **Amidation site.**

amino acids 68-72

#### **Small cytokines (intecrine/chemokine).**

amino acids 23-88



# FIGURE 17

GCGAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTCGATCCACCCCTCC  
TCCCTTCTC**AT**GGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC  
CAGGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCTCTTCATCGTCGCGG  
TTCTGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG  
TAACCCGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGT'T'  
GTAAATCAGGTCAAACAAATAAAAGTTCTGTACCACGACCAGAGACACCGTGTGTGAGTGTGAAAAAGGAAGC  
TTCCAGGATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGAGGGATGGTCAAGGTCAG  
TAATTGTACGCCCCGGAGTGACATCAAGTGCAAAAAATGAATCAGCTGCCAGTTCCTACTGGGAAAACCCAGCAG  
CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA  
GTCATCATTTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTG  
CTCAGGTGGTGGAGGAGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGGCGTTCATGTCTTTCACGAGTTC  
CTGGGGCGGAGGACAATGCCCGCAACGAGACCCCTGAGTAACAGATACCTTGCAGCCACCCAGGTCTCTGAGCAG  
GAAATCCAAGGTCAAGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTGCAGAGGAGGCCACAGCGTCTGCT  
GGAACAGGCAGAAAGCTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA  
TCAGCACCTTGCTGGATGCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAGGACCAACTGGTG  
GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTG**TGA**AAGAATCTCTTCAG  
GAAACCAGAGCTTCCCTCATTTACCTTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGA  
CCCATGCCCAACAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCCTAGAACTTTGTTAACGCACCT  
GGAGTAATTTTTATGAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT  
TATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAG  
GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAGTCCATCTCAAT  
TTAAAAAGAAAAAAGTGGTTTTAGGATGTCATTCTTTGCAGTTCCTTCATCATGAGACAAGTCTTTTTTCTGC  
TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGCCAC  
AATGCTTTGCCTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTCAGTTTCGGATA  
TTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTC  
GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTG  
CTTACTACTGTAGGCTGTACATCTCTTTTCCGATTTTTGTATAATGATGTAAACATGGAAAAACTTTAGGAAAT  
GCACTTATTAGGCTGTTTACATGGGTGCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGT  
GACGAGGGAGAAATCCTCCCTCTGTGGGAGGCACTTACTGCATTCCAGTTCCTCCCTCCTGCGCCCTGAGACTG  
GACCAGGGTTTTGATGGCTGGCAGCTTCTCAAGGGGCGAGCTTGTCTTACTTGTTAATTTTAGAGGTATATAGCCA  
TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC  
CTGGTATCTTTGGGAAGCCATGTGTCTGGTTTGTCTGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTC  
CACAGCAGATGAGGACAGTGAGAATTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACA  
GTTGAACGTTAGTGAATCTTGAGCCTCATT'TGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCC  
ATGGCATCAAGAGGGGAAGAGTGGACGGTGCTTGGGAATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGC  
CCCTCTCGCTTCTGGTGGTCTGTGAAGTGAAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTT  
TAGGGTACAGATTCCCTGTTTGGAGAGCTTGGCCCTCTGTAAAGCATCTGACTCATCTCAGAGATATCAATTCT  
TAAACACTGTGACAACGGGATCTAAATGGCTGACACATTTGTCTTGTGTACGTTCCATTATTTTATTTAAA  
AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCTTCTCCACAGTAGCCAGTCCGTGGTAGGATAAATTA  
CGGATATAGTCATTCTAGGGGTTTCAGTCTTTCCATCTCAAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTTG  
GCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTAGATTGTTGTGTCCATGGAGTTTTAGGAGGGGATG  
GCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCCACACCTTGTCCCCTGCACTTCTG  
GATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCTTTGCTGGGCCTTCTGTGCAGGAGACTTGGTCTCAAAG  
CTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT  
ACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTCTTGACAACATGAAATGTTGGGGTTTTTT  
GGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAATAGCACATAACACCTGGTTATATATGAAA  
TACTCATATGTTTATGACCAAAATAAATATGAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 18**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD  
 EVPQQTIVAPQQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG  
 QTNKSSCTTTRDTCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA  
 SSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIILAVVVVGFSCRKKFISYLKGICSGGG  
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAEALTGVTVES  
 PEEPQRLLEQAEAEGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL  
 FYEEDEAGSATSCL

**Important features of the protein:****Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,  
 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

**FIGURE 19**

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAAGTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

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## **FIGURE 20**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation sites.**

amino acids 120-124, 208-212

#### **Glycosaminoglycan attachment site.**

amino acids 80-84

#### **N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

**FIGURE 21**

CCGGGGAGGGGAGGGCCCCGTCCCCGCCCTCCCCGTCTCTCCCCGCCCTCCCCGTCCCTCCC  
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGGCTGCCCTC  
TGCCCGGGTTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG  
TTCGTGGCGCTACCCGCCCTCCGGCTGGCTGACGACGGGCGCCCCCGAGCCGCCGCCGCTGTC  
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAAC TAACTGAAAGATGATGGGGACATAT  
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA  
CCTGTAAATAGTGGTGTAAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT  
TGAAAATTTGGAGGAAAAAGAATATTTTGGGAATTGTCAGTGTAAAGGATTTTAGTTCATGAGT  
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT  
GATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGATATTTTAGTTAAGAACCGGGG  
AGTACTCAGACATTCAAAC TATACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC  
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCACTG  
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC  
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC  
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTTCCCAGTATTC  
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT  
AAAGGTGTTTTTCCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGGACGTCA  
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA  
GATAAACATGTATTTTAAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC  
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

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## **FIGURE 22**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRSDIL
FTLPNLSKKESVSSLQTTTSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPKEKRAENLEDKTCI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 266-284

#### **Leucine zipper pattern.**

amino acids 155-176

#### **N-glycosylation sites.**

amino acids 46-49, 64-67, 166-169, 191-194

**FIGURE 23**

CGTCTCTGCGTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG  
CCCTGGCTTGGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT  
GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC  
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG  
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCTACTGCCTTCCCTGCAAAGATTCTG  
TGCACGGCGTGGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCCGCGCTG  
CGAGTGCGCGCCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG  
CCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC  
GTCATGTACCGGGGCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC  
GTGCGTTCGTGGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGGCGCCCTGCCCTG  
TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGC  
CACATGCGCCAGGCCACCTGCTTCCTGGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG  
CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAAGTCTGCAGAAGAGGAAGAGAACTTCGTG**T**  
**GAG**CCTGCAGGACAGGCCTGGGCCTGGTGCCCGAGGCCCCCATCATCCCCTGTTATTTATT  
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTT  
GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCC  
GGCTGGTGGGTGGGATAGACCTGCGTTCGGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT  
AGGATGCCCCAGCCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT  
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT  
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT  
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG  
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG  
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG  
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG  
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGA  
CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC  
CACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT  
CCTGTGAAGGCCATTGAGAAATGCCCAGTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCC  
TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGTCCACGTTCAG  
TTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGACGCTCAGAGCAGGGC  
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACACAGGGCCACTGC  
TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT  
CCTGGAGCCGGGTGTCCCAGTGGCACCACTAGGTGCCTGCTGCCTCCACAGTGGGGTTCACA  
CCCAGGGCTCCTTGGTCCCCCACAACTGCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC  
AGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG  
CCAGTTCTCCACGACGGCTCACCCCTCCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC  
TGTGCCTGCGTGTAACACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT  
CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC  
CAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAAAGTGCCCTAGGTTGGTGGGTCTA  
CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAAATAAAGA  
CTCAAGCCATAAAAAAAA

**FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGFLWPLPWGALAWAVGFVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC  
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPD  
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDQ  
TGSAHCVVCRAAPCFVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE  
EPPGGESAEEEEENFV

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202



**FIGURE 25**

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT  
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT  
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA  
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTGCGGGGGCCGCCTGGCTA  
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCATCCATCCTTTAAATCTG  
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTCAAGCCTCTGGTGGCCTACT  
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA  
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG  
TTAGACAAGTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGA  
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTG  
AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG  
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCAGTGTCTTG  
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC  
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC  
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTCTG  
TTCAGACTTCTATGACATCGTCTTGTTGGCCACTCCGTTGAATCGAAAAATGTGAATATTA  
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACA  
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGG  
CCTTAATACAGTTTTAACCCTGATAATTCAGATTTGTTTCAATTAACAGTATTGGGATTGTGC  
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAAGATC  
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGC  
TGTGAAGAAGCCATGGCTTGCATATCCTCACTATAAGCCCCGGAGAAATGCCCCTCTATCA  
TTCTCCATGATCGACTTTATTACCTCAATGGCATAAGAGTGTGCAGCAAGTGCCATGGAGATG  
AGTGCCATTGCAGCCCACAACGCTGCACTCCTTGCTTATCACCGCTGGAACGGGCACACAGA  
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACTAT**TGA**AGTGACACACTCC  
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAGAACAAAATCTGAGCAGAGA  
TGATTTTGAACCAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT  
AGGAAAAA

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCEGAELRAPD KIAIIGAGIGGTS AAYYLRQKFGKDVK  
IDLFEREEVGGRLATMMVQGGQEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE  
TLVFEE SNWFIINVIKLVWRYGFQSLRMH MWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL  
GGDDFLGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW  
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDI  
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLT  
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWL  
AYPHYKPPEKCP SII LHDRLYYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG  
LYEKLKTEL

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 196-200, 323-327, 353-357

**Tyrosine kinase phosphorylation site.**

amino acids 291-298

**N-myristoylation sites.**

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,  
119-125, 260-266, 384-390, 459-465

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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## **FIGURE 27**

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT  
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG  
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT  
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT  
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG  
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT  
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT  
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG  
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTATAA  
GAGATGATGGAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA  
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA  
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTTAAATCTGA

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## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKKPL  
MVIHHLEDCQYSQALKKVFAQNEEQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP  
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-myristoylation site.**

amino acids 51-57

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## **FIGURE 29**

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA  
AAGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGA  
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG  
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCGCCACTTCCAC  
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT  
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG  
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAA  
AACAAATGTAATTGAAATAGCACACAGCATTTCTCTAGTCAATATCTTTAGTGATCTTCTTTA  
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

amino acids 47-85

## FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGGCGGCGGGC**ATG**GGGCCGGGGGCCCTGGGAT  
GCGGGCCCCGTCTCGCCGCCTGCTGCCGCTGTTGCTGCTGCTCGGCCTGGCCCCGCGGCGCCGC  
GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC  
AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT  
CAGTGTGTTGATAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACACACATC  
TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCTGGAAGGATATCGAGCCACAAACA  
ACAACAAGACATTTCATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT  
TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG  
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT  
CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT  
TATACGTCTAGTCTGGGCAGCCAGGTTTCGTTATGCTTGCAGAGAAGGATTCTTCAGTGTTC  
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC  
AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC  
TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA  
GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA  
TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC  
TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC  
TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCAGAAAGTGT  
GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC  
TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG  
TTTCAATATTTCAATATTTAATGAACTTGTTTGAATTTGAACAGGCGTTCTAGGAAAGTTG  
GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGGTGGTATCTGGCTAACTTTTCT  
CATGCAACATCGTTTAACTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA  
CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACTCAGTGC  
AAATAACAATAGCAACTCCCCAGCAGTAAAACAGACCATCAGTAACATTTAGGATTTAAT  
GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTTCCA  
CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCAGGAAATGACCTTTAATATCAGTA  
GCAGCAGCCGAGATCCCGAGGTGTGCTTGACCTACGTCCGGGTACCAACTACAATGTCAGT  
CTCCGGGCTCTGTCTTCGGAACCTCCTGTGCTCATCTCCCTGACAACCCAGATAACAGAGCC  
TCCCCTCCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA  
GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCCTGGCC  
CTCCAAAGCACATTTTCTTGATTTCTGAAGGCGCTTCCTCCTTCTTTAGCAACGCCTCTGA  
TGCTGATAGGATAGCTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA  
TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCTTGAAAAGAGGGAGT  
GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC  
AGTTTGGGCTCAGGTGAAAGATTTCGTCACCTCATGCTGCTGCAGATGGCGGGTGTGGACTGG  
GTTCCCTGGCTGTTGTGATCATTCTCACATTCCTCTCCTTCTCAGCGGT**GTTGA**TGGCAGATG  
GACACTGAGTGGGGAGGATGCACCTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC  
GCACAGAGGCTCCGTGTGACTTCCTGCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC  
CAGCTGGGCCCCATTCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA  
AACTCAGGAATTCTGAGTCTTCCCTGCTACAGGACCAGTTCTGTGCAATGAACTTGAGACT  
CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC  
TTCTCTGAGTGTGCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA  
ACCTCCTATATAAAAGCATTTCTGTAAATTCATTGAGAATCCATTCTTTACAATATGCAGTG  
AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTCAATTGAAAAAGAGAACA  
GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCTTATAAATTAGTTGATAT  
ACTAATGAGAAAATATACTAGCCTGGCCATGCCAATAAGTTTCTGCTGTGTCTGTAGGCA  
GCATTGCTTTGATGCAATTTCTATTGTCTATATATTCAAAGTAATGTCTACATTCCAGTA  
AAAATATCCCGTAATTAAAAA

**FIGURE 32**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQREGKKICICNYG
FVGNGRTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNNKTFIPNDGTFTCT
DIDECEVSGLCRHGGRCVNTHGSEFECYCMDGYLPRNGPEPFHPTTDTATSCTEIDCGTPPEVP
DGYIIGNYTSSLGSQLVRYACREGFFSVPEDTVSSCTGLGTWESPCLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKG TWRESTLTCTEILTKINDVSLFNDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPPRRSMPAVIGFQTAEVDLLEDDGSFNISIFNETCLKLNRRSRKVGSEHMYQFTVLGQR
WYLANFESHATSFNFTTREQVPVVC LDLYPTTDYTVNVTLRLSPKRHSVQITITPPAVKQTI
SNISGFNETCLRWSIKTADMEEMYLEFHIWGQRWYQKEFAQEMTFNISSSSRDPEVCLDLRP
GTNYNVSLRALSSSELPVVISLTTQITEPPLPEVEFFT VHRGPLRLRLRKAKEKNGPISSYQ
VLVLPLALQSTFSCDSEGASSFFSNASDADGYVAAELLA KDVPDDAMEIPIGDRLYYGEYYN
APLKRGS DYCIILRITSEWNKVRRHSCAVWAQVKDSSLM LLQMAGVGLGSLAVV IILTFLSF
SAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 718-740

**N-glycosylation sites.**

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 478-482, 686-690, 705-709

**Tyrosine kinase phosphorylation site.**

amino acids 419-427

**N-myristoylation sites.**

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126, 146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694, 727-733.

**Amidation site.**

amino acids 52-56

**Aspartic acid and asparagine hydroxylation sites.**

amino acids 91-103, 141-153.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 624-635

**Cytochrome c family heme-binding site signature.**

amino acids 39-45

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 85-106, 135-156

**Receptor tyrosine kinase class V proteins:**

amino acids 389-422



## FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
TGCCCGCTATGACTCTAGCACCGGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
ACCTCTTCTAGGGCCTCAACCCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC  
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA  
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC  
ACCCCGTCAACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC  
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT  
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCCTCAGA  
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC  
ACAGCCGGCACCCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA  
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTT  
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCCT  
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCCGGAC  
GAGGCCGACCACAGACG**TGAG**TGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG  
TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
CGGGAACCTCCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCCTAGCCTG  
GGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
AAGGGCAGCATGTCCAAGCCCCTAACCCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC  
CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCCAGAGGTGTCCTTGGACTCACCTTGG  
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
TTAAAATTCACCTCAGTGTGGCCCCAAAAAAA

## FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
SAETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAI FDTLCTDD SSEEAKTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSIEAGSAVGKTTSEAGSSASSYSPSEAALKNFETPSETPTMDIATKGPFPTSRD
PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-25

#### N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

#### N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,  
314-320, 349-355, 386-392, 397-403, 449-455

#### ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

**FIGURE 35**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG  
GCCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA  
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC  
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCA  
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT  
ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT  
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA  
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA  
ACTGGCTCTGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA  
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT  
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTCTGGGTTATTCCTGGAGATACTGGT  
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT  
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGG  
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA  
GCTATTCATTAACTTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTCA  
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT  
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT  
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC  
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAAT  
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAACTACCTATCTGGTTTATGACCACTTA  
GATCGAAATGTC

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## **FIGURE 36**

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAA  
TTGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL  
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRVWPWPQGAVHFNLLDV  
AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTNLNPDQCHPSRK  
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNY  
AFMQALMHAVDPEIPQAVCIPTKLSPISMYQDNNDNVILRHYEDMVVDECGCG

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 112-116, 306-310

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

#### **N-myristoylation site.**

amino acids 77-83

#### **TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

## FIGURE 37

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC  
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
TGCTCTAGGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC  
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTGGCTTCTGGCTGGT  
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG  
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC  
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG  
ATCGAGGCCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA  
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTTTCGGTGGGCGGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG  
ACACGGAGTTCTGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTAC  
GTGCCCCGGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC  
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG  
TGGCTACCTGGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC  
CCTGGCTTTGGCATTTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC  
GAGAACCCTCTGGGACCTTCCGCGGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC  
GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCCCTTGAAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGAGGACAAAGAAAAGGG  
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT  
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGACCCCTGGGTCCCCCA  
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT  
TTCTGTGCGCCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCCTTGGCTTCTGTTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT  
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT  
CATCCAGGCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTTCAGAGCAGGGGAGAG  
CTGGAAGGGGCTAGAAAGCTCCCGCTTGCTGTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCAATCACCCGTGTCAGGATTCAGTCTCAGGAGC  
TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC  
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC  
GCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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## **FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP
```

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

**FIGURE 39**

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA  
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATG**GCTG  
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT  
GACACTCAAGAGCTACGATGTCTGTGTATTTCAGGAACACTCTGAATTCATTCCTCTCAAAC  
CATTA AAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG  
TCCCAAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT  
GGCCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT  
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTTCATTTGGGAGACCTGAGA  
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC  
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**  
**AA**AGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA  
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT  
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTTACAGGTGACTGCTCCCCCAT  
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT  
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG  
TGCATCTCGGTGTAGAGCAAGGCTCCTTGCTTTCAGTGCCCCAGGGTGAAATACTTCTTTGA  
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

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## **FIGURE 40**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIK NIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFP PAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation site.**

amino acids 68-72

#### **N-myristoylation site.**

amino acids 69-75

#### **Small cytokines (intercrine/chemokine) C-x-C subfamily signature**

amino acids 40-85



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## FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC  
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT  
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG  
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC  
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG  
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA  
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG  
GAGACCCCACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG  
CTCAGGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC  
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC  
AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCCT  
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT  
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCA



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## FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT  
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG  
 ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA  
 TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
 TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
 AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
 ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
 CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT  
 GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
 CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

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## **FIGURE 44**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSEFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

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## FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGCGGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGA  
CAAGAAGCCGCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTCGCCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAG**TAA**CT  
GAGACCATGCCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTACAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTTCCC  
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACCTTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGT

## **FIGURE 46**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI  
 RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE  
 EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
 MFSSPLETDSMDPFGLVTGLEAVRSPSEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

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## FIGURE 47

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTTGGTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAA  
GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCTACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 48**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW  
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFEKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



[illegible]



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## FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACC GAACCTGACAAAAAAGAAGAAAAAGAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACCTACACTTGCCTGGCCTCCAACAAGCTGGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

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## **FIGURE 52**

MKTIQPKMHNSISWAIIFTGLAALCLFQGVFVRSGDATEFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTLOCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

**Signal peptide:**

amino acids 1-28

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**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM  
 NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSGNSGGSRGDSGSESSW  
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL  
 GGSGDNYRGQGSSWGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
 RSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

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## **FIGURE 55**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGAC  
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT  
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
**ATAG**ACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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## **FIGURE 56**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAPLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90



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## **FIGURE 57**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
C**ATG**ATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCCACCCTCAACCAATATCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA

**FIGURE 58**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWKSSDTISKNGTL  
SSVTSARALRPPHGP RP GAL TPTPSLSSQALPSRPLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
 GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTTCTTTTTTCCCACCACATTGTATTTTAT  
 TTCCGTACTTCAGAAATGAGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCCT  
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
 TGGATTTCTTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
 AACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTGAGAGTTCTCCATTTGCAGGAAAC  
 AATATTCAGACCATTTCACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
 TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTGCATATCCGACATGGCCTTCCAGAA  
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC  
 CACCCTCCTCCCAGTCTCCCAGTACGTCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
 AAACCAACTTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
 ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG  
 CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC  
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACCGTGATGGCATA  
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
 CCAGAAGTGGAAATACAACCGGGGCGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
 AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
 CAACTCCTTAAAGGAGATTTTCACTGACAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
 CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
 ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTCTTTGCTTTTTTAAATCTT

## FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
 SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
 PWFCDCSIKWWTEWLKYIPSSLNVRGFMCGPEQVRGMARELNMNLLSCPTTTPGLPLFTP  
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPI SERIQLSIHVND  
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHL SLVNLEPRSTYRICLVPL  
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
 DFERLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
 522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCA**ATG**AACTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACTTTTCTGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT  
GATTTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA  
AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACCTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTGA  
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAGTGTTCATCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTTGACTAATAGAAGTGGTTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGCAATTATGATCATA  
TTTGGGTTTTATTTTTTTGACTTTGGGTTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTTCAAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAAT**TAGG**  
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCAATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG  
TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT  
TTAAA

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## **FIGURE 62**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKT TSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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## FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCA**ATGGC**  
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC  
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC  
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG  
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA  
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTC  
CCTCAATCTGATAGGTTCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG  
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA  
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG  
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTT**TGA**CCAGAGCAAAGCTGAAAAATGAA  
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC  
CAAAGGAAGATGGGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT  
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA  
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT  
TTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC  
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA  
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG  
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC  
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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## **FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185

><subunit 1 of 1, 179 aa, 1 stop

><MW: 20011, pI: 8.10, NX(S/T): 3

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE  
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPOSDRFQPYMQEVPFLAR  
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

#### **N-myristoylation sites.**

amino acids 14-20, 82-88

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21



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## FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCGAGAAAGGA  
CGCGCGCCCTGCGTCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCATCAAC  
CTCCTTCCCAGCAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA  
GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT  
TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACCGGGTTGG  
CGCTGCCCCGAGTGGAAACCGACAGTTTGCAGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG  
GTTGTTGTTTCAAGTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGG  
TCCGAAGAGCGCTGCGCTCCTACTCGCGTTTCGCTTCTTCTCCTCTTCTCGGTTCCCTACTGTGA  
AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTACCGAGACCGATCCGCGAGCGTTTGGCC  
CGGTGCTGCCTATTGCATCGGGAGCCCCCGAGCACCGGCGAAATGGCGAGGTTCCCGAAGGC  
CGACCTGGCCGCTGCAGGAGTTATGTTACTTTTGCCACTTCTTCACGGACAGTTTCAGTTCG  
CCGATGGGAAACCCGGAGACCAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT  
CACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCACAGGTGGAAAAGAACTT  
GGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA  
GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT  
ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT  
ATGGGTGAACATAGACCAAATGGAAGATAAAGTGAAGATTTCATGGAATATGTCCAATA  
CTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCCATTTTATGGCCACTTCCTA  
CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT  
AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCAGTGTATCCAGAAATT  
CAACTGTCAGATATTTTGTATAATGGCACAGCATTGTGGTCCAGTGGGACCATGTACATCTC  
CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCCTGCTCATGGATGGACGAAT  
CATCTTTGGATACAAAGAAATTCCTGTCTTGGTTCACACAGATAAGTTCAACCAATCATCCAG  
TGAAAGTCGGACTGTCCGATGCATTTGTCTGTTGTCCACAGGATCCAACAAATTCCCAATGTT  
CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT  
TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAACAGATGTGGCCCCCTGTG  
TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGA  
TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGAAGAT  
GTGTGAGAATACAGAACCAGTGGAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA  
CCACCCAGTTTCAGGGTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC  
CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA  
TGACAGTGCAGCTGAGAAGAAAGGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCA  
TCCTGGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA  
TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAG  
AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAGTTGGAGAGAAAGAAGGCTTTA  
TTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAACACCAGTACTGGTTTACAGGTGT  
TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACAAACACACACAAACAAGCTC  
TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAACAAAGGG  
TAAACAAAAAACTAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCCTAGTGG  
AATGTATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA  
TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC  
TTTAGTTCATGAGGG

**FIGURE 66**

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTTQAFPHTEEEVEVD SHAYS  
 HRWKRNLDLFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYYSISRIYGPS  
 DSASRDLWVNI DQMEKDKVKI HGILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTG  
 EVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVLQDNYNLGSFTFQAT  
 LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTTIYEYHRVELQ  
 MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCP  
 EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK  
 DNGASTDDSAAEKKGGLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR  
 WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

**Important features of the protein:****Transmembrane domain:**

amino acids 454-478

**N-glycosylation sites.**

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 297-301, 492-496, 503-507

**N-myristoylation sites.**

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,  
 455-461

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## FIGURE 67A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTG  
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGA  
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG  
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCTTGGCTGAACCGGTCAAGTATTAT  
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA  
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT  
GTTTCAGACTCAACATACACCCAGAACATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAA  
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT  
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA  
TTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA  
ATGCAGTGCAGGAAATGATGTGTCATTCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACT  
TTGCTCCTACTATTTCAGGAAATTAAATCTGGCACCGTGACCCCGGACGCAGTGGCCTGATA  
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT  
CTTCAATGGCCAACAAGGAATTATTATTTCAAATTTTAGCACAAAGATCCATTCTCACTGTTA  
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA  
ACCAATGCGAGCCTGCCTCTTAACCTCCAAGTACAGCCAGTATGGAATTACCGGGAGCGC  
TGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCTCTTTTACCAGCATATTCT  
ACCTGAAGAATGCCATTCTACAATAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT  
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAGCAGCGTGGGATATAATC  
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT  
TCTACTCTTTTTTGATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCTCTTTTTTTAAG  
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTCATTGTTGTAATCTAC  
AACTTTTCAAAGCATTTCAGTCATGGTCTGCTAGTTGCAGGCTGTAGTTTACAAAAACGAA  
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCTGTTTCAAT  
AAGTCAATCCACATTTACAAAGATGCATTTTTTTTTCTTTTTTGATAAAAAAGCAAATAATA  
TTGCCCTCAGATTATTTTCTTCAAATATAACACATATCTAGATTTTTTCTGCTCGCATGATAT  
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTGT  
AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAACATAATAA  
AATGTTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCA  
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA  
TGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC  
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA  
AATCATTCCCTTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT  
TTTCTTTTCACTAGTCCAAGCCAAAAATTTTAAAGATGATTTGTGAGAAAGGGCACAAAGTCC  
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGTGGCAGCTAA  
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA  
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAAACCTTCCAAAATATATTA  
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA  
AATCTTTCTATATAGCCATTTTCAGTGCAAACAAGTAAAATCAAAAAAGACCATCCTTTATTT  
TTCTTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT  
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA  
AACTACATTTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG  
TTTCACTCTTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT  
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAAG  
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG  
TATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTTTTTTCTTCAAGTAAACTTAGT  
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG  
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT  
AAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTGAACAAATATGGCATT  
TAACCTTTATTATTTATTTGCTTTTAAAGAAATATTCTTTGTGGAATTGTTGAATAAACTATAA  
AATATTATTTTGTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

# **FIGURE 67B**

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC  
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT  
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG  
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT  
CAGTAGCTATATGTATTTGCCCTTATGTTAGAAGAGACTTTCTTGAGTGACATTTTTTAAATA  
GAGGAGGTATTCACTATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA  
CAGAGTGAAATCATGAGTATTTATGAGTTCATATTGTCAAATAAGGCTACAGTATTTGCTT  
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA  
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG  
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTCAATTCAGG  
ANTATATTTTCTACAAGTTCCACTGTGGGACTCCTTTTGTGGCCCTATTTTTTTTTTAAAG  
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG  
AAAAGGAAAGGCAGTAAAGAGGGGAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG  
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG  
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAACTATGTTTTTCAA  
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT  
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG  
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG  
CTTCATCATAACATTTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG  
GTAATTCAGGGGAAAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA  
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG  
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA  
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA  
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA  
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA  
CATCCATATTTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC  
TCAGTTTATCAATTAATAA

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## **FIGURE 68**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259

><subunit 1 of 1, 354 aa, 1 stop

><MW: 38719, pI: 6.12, NX(S/T): 6

MDMMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL  
EDGASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQH  
TPRTMQVHLTVQVPPK IYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQ  
YLDIYGITRDQAGEYECSAENDVSFPDVRKV KVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA  
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL  
PLNPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 322-343

**N-glycosylation sites.**

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

**Tyrosine kinase phosphorylation site.**

amino acids 180-188

**N-myristoylation sites.**

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,  
304-310, 321-327

**Myelin P0 protein.**

amino acids 94-123

## FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA  
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTG  
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA  
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT  
TTAATTAAGGGGTTACATCCAACCCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT  
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAA  
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA  
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA  
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC  
CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG  
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAG  
GCCAGTGCCGGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC  
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCT  
TCTCCTCCTGCAAATAG

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## **FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK
```

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 51-69

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

#### **N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

#### **Amidation site.**

amino acids 33-37

## FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCATGGCGTGGAGCCTTGGGA  
GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC  
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG  
GAACCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA  
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC  
AGGGCTGAATTTGCAGATGAGCATTGAGCTGGGTAAACATCACCTTCTGTCTGTGGATGA  
CACCATTATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT  
TCTTAGCCCCCTAAAATTGAGAATGAATACGAACTTGGAATATGAAGAATGTGTATAACTCA  
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA  
GTATGACTTTGAGGTCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAG  
GGTTTCTTCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC  
CATGACGAAACGGTCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT  
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCGTTTACAAGAAGACAAAGTACG  
CCTTCTCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT  
AACACACTTCTGTTTTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAG  
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA  
CCCCGCCTGGGCAGGGGCCCCAAAGCTAGGCTCTGAGAAGGAAACACACTCGGCTGGGCACA  
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA  
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT  
TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCA  
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA  
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA  
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA  
TGGTGAAACCCAGTCTCTACTAAAAATACAAAATTAGCTAGGCATGATGGCGCATGCCTAT  
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA  
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT  
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAAATGAGGAATAAGAATGG  
AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG  
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGATTCTTTGCA  
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGCTCCATTAAAGT  
TTTACTCTGTGTTGC



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## **FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWT
YCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPSWMVAVILMASVFMVCLALLGCFSLWCV
YKKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP
DSCSLGTPPGQGPQS
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 222-245

#### **N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

#### **N-myristoylation sites.**

amino acids 6-12, 316-322

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## FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCCGCTCGCCGCCCGCC**ATG**GCCC  
GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCCGCTGCTGGCGGAGAT  
GCCCCGCCGGGCAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT  
TCTCCAGCAGCACTTTGGACCTCGGGTGACAGTCGACGTGTACGAGAAGGGAACCGTGGGTG  
GCCGCTTGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC  
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT  
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC  
TGCTGAACCTCTTCCGCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG  
GTGGAGGAGGTGATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT  
CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTTAACATGACCCAGC  
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTATTGATGATGTCTGTT  
TCTGCTGTCTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAGGAGCCAT  
GTCACTAGCCGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT  
CCGGTTTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTACCTCTGTGACCCTG  
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC  
TGACTTCTATGACATCGTGGTCAATCGCCACCCCGCTGACCTGGACAACAGCAGCAGCAACT  
TAACCTTTGCAGGCTTCCACCCGCCCATTTGATGACGTGCAGGGCTCTTTCAGCCACCGTC  
GTCTCCTTGGTCCACGGCTACCTCACTCGTCTTCTTCCGGTTTCCCAGACCCTAAGCTTTT  
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT  
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA  
GTCCAGTCCCCCAAGCCCTCTTTCGGACCCAGCTAAAGACCCTGTTCCGTTTCTTACTC  
AGTGCAGACAGCTGAGTGGCAGGCCATCCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT  
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG  
GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT  
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAACTGTGAGGGCTCTAGG  
GAGAGCCTGGGAACCTTTCATCCCCCACTGAAGATGGATCATCCACAGCAGCCAGGACTGA  
ATAAGCCATGCTCGCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG  
ACCTACTGTCTGCTTATATTAAGGGTCCACACGGCGGCTGCTGCTTTTTTTTTTAAGGGGGAAA  
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTTAAGAAGAA  
AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAGAAGACTACG  
GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC  
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA  
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT  
TGATGGATTTGAAGTACCTAGTTCAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC  
ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC  
GTCACCATATCTCCAAGCTTCCCTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA  
GAGGGAAGCTCTTCCCTGGCACCTAGAGGAATTAGCCATTCTCTTCCCTTATGCAAAGATTGA  
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC  
TAGATGTTTCATCCCAGCAGAAGAAAGAAGAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC  
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT  
TTCTACAAACCCTTAAAAATCACTTGTTTTAAAAAGAAAGTAAAGCCCTTTTCATTCAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 74**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAAPLLAALTALLAAAAAGGDAPPKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGGRLATISVNBKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVVSAVLRASYGQSAAMPAFAGAMSLAGAQQSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYNSSYFGFPDPKLFPPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAAVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPYGSRPTEL
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLDKIDQKDLMHKVKTEL
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

#### **N-myristoylation sites.**

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,  
237-243, 429-435